This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

1. (currently amended) A method for generating a molecular profile of genomic DNA by hybridization of a genomic DNA target to a plurality of immobilized nucleic acid probes, wherein the plurality is a collection of clones that represent all of a chromosome or a genome of an organism, the method comprising:

(a) providing the plurality of nucleic acid probes comprising a plurality of immobilized nucleic acid segments in an array with each probe at a known location, wherein each probe is a member of a genomic library cloned in a vector and each probe is the vector having a cloned nucleic acid insert greater than ~~about~~ 50 kilobases, wherein the plurality of probes represents all of the chromosome or the genome;

(b) contacting the immobilized probes with a sample of target nucleic acid comprising fragments of genomic nucleic acid,

wherein said fragments include both strands of a double-stranded genomic DNA fragment and include at least 30% repetitive sequences, and

wherein both strands are labeled with a detectable moiety, wherein each labeled fragment consists of a length smaller than ~~about~~ 200 bases, and the contacting is under conditions allowing specific hybridization of both strands of the labeled fragment of the target nucleic acid to the probe nucleic acid; and

(c) observing an amount and location of labeled genomic nucleic acid hybridized to each immobilized probe, to detect regions of amplification or deletion in the sample, wherein positional information of clones on the arrays and chromosomes is correlated,

wherein said method results in less aggregating hybridization to said probes relative to hybridization of said target genomic nucleic acid to said probes using target nucleic acids with labeled fragments of length greater than ~~about~~ 200 bases,

or said method results in less background relative to hybridization of said target genomic nucleic acid using target nucleic acids with labeled fragments of length greater than ~~about~~ 200 bases,

thereby generating a molecular profile of the chromosome or genome of the sample genomic nucleic acid.

2. (currently amended) The method of claim 1, wherein each labeled fragment consists of a length no more than ~~about~~ 150 bases.

3. (currently amended) The method of claim 2, wherein each labeled fragment consists of a length no more than ~~about~~ 100 bases.

4. (currently amended) The method of claim 3, wherein each labeled fragment consists of a length no more than ~~about~~ 50 bases.

5. (currently amended) The method of claim 4, wherein each labeled fragment consists of a length no more than ~~about~~ 30 bases.

6. (previously presented) The method of claim 2, wherein each labeled fragment consists of a length between about 30 bases and about 150 bases.

7. (previously presented) The method of claim 1, wherein the sample of target genomic nucleic acid is prepared using a procedure selected from the group consisting of random priming, nick translation, and amplification, of a sample of genomic nucleic acid to generate segments of target genomic nucleic acid; followed by a step comprising fragmentation or enzymatic digestion, or both, of the segments to generate a sample of target genomic nucleic acid consisting of sizes smaller than about 200 bases.

8. (previously presented) The method of claim 7, wherein the random priming, nick translation, or amplification, of the sample of genomic nucleic acid to generate segments of target genomic nucleic acid incorporates detectably labeled base pairs into the segments.

9. (previously presented) The method of claim 8, wherein the detectable label comprises Cy3™ or Cy5™.

10. (previously presented) The method of claim 1, further comprising prior to step (b), fragmenting the sample of target genomic nucleic acid to sizes smaller than about 200 bases by DNase enzyme digestion.

11. (previously presented) The method of claim 1, further comprising prior to step (b), fragmenting the sample of target genomic nucleic acid to sizes smaller than about 200 bases by applying shearing forces sufficient to fragment genomic DNA followed by DNase enzyme digestion of the sheared DNA.

12. (original) The method of claim 1, wherein the conditions allowing hybridization of the target nucleic acid to the probe nucleic acid comprise stringent hybridization conditions.

13. (original) The method of claim 12, wherein the stringent hybridization conditions comprise a temperature of about 60°C to about 65°C.

14. (original) The method of claim 1, wherein the target nucleic acid consists essentially of DNA derived from a human.

Claims 15-16 (canceled)

17. (previously presented) The method of claim 1, wherein the chromosome or genome is derived from a human.

Claims 18-66 (canceled)

67. (previously presented) The method of claim 72, wherein the sample of target genomic nucleic acid consists essentially of one chromosome.

68. (previously presented) The method of claim 72, wherein the sample of target genomic nucleic acid comprises a complete genome.

Claim 69 (cancelled)

70. (previously presented) The method of claim 1, wherein said method results in less aggregating hybridization to said probes relative to hybridization of said target genomic nucleic acid using target nucleic acids with labeled fragments of length greater than about 200 bases.

71. (previously presented) The method of claim 1, wherein said method results in less background relative to hybridization of said target genomic nucleic acid using target nucleic acids with labeled fragments of length greater than about 200 bases.

72. (previously presented) The method of claim 1, wherein said fragments of genomic nucleic acid comprise nucleic acids from all of one or more chromosomes of said organism.